

## LETTER TO THE EDITOR

Generation of the *Fip111–Pdgfra* fusion gene using CRISPR/Cas genome editing

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The *FIP1L1–PDGFRA* fusion gene is an important oncogenic driver of chronic eosinophilic leukemia, now referred to as the WHO subcategory 'myeloid and lymphoid neoplasms with eosinophilia and abnormalities of *PDGFRA*, *PDGFRB* or *FGFR1*'.<sup>1,2</sup> The *FIP1L1–PDGFRA* fusion is generated by a 800-kb chromosomal deletion, unlike the majority of other fusion genes that are generated by chromosomal translocations. The resulting *FIP1L1–PDGFRA* protein (Figure 1a) is a constitutive active tyrosine kinase that is highly sensitive to the kinase inhibitor imatinib, and treatment with this drug results in rapid complete remission for *FIP1L1–PDGFRA* positive patients.<sup>3</sup> Although the response to imatinib is excellent, most patients require life-long treatment and the development of resistance has been described in some cases.<sup>1,4,5</sup>

Most of our insight into the mechanism of activation of the *FIP1L1–PDGFRA* kinase, its downstream signaling and its sensitivity to kinase inhibitors has been obtained from studies using ectopic overexpression of the recombinant fusion protein in Ba/F3 cells or other cell lines such as HEK293T. The interleukin-3 (IL-3)-dependent Ba/F3 cell line has been widely used to study oncogenic tyrosine kinases, since many constitutively activated tyrosine kinases can transform the Ba/F3 cells to IL-3-independent growth.<sup>1,6,7</sup> It is at present unknown if the data obtained from such overexpression experiments is completely valid and if it accurately resembles the actual situation in the leukemia cells in which there is only one copy of the *FIP1L1–PDGFRA* gene driven by the *FIP1L1* promoter.

To address this question, we used CRISPR/Cas genome editing to generate the *Fip111–Pdgfra* fusion gene by inducing a 600-kb interstitial chromosomal deletion in the Ba/F3 cell line.<sup>8</sup> We designed six different guide RNAs (gRNAs) targeting exons 9, 10, 11 or 12 of *Fip111* and three different gRNAs targeting exon 12 of *Pdgfra*, reflecting similar breakpoints found in *FIP1L1–PDGFRA* positive patients<sup>1</sup> (Figure 1b). The design tool developed by the Zhang lab (crispr.mit.edu) was used to find gRNAs with minimal off-target effects.<sup>9</sup> gRNA sequences were cloned into a plasmid (pX330) carrying a Cas9 expression cassette, and this plasmid was delivered into Ba/F3 cells by electroporation. The targeting efficiency of the individual gRNAs in Ba/F3 cells was determined using next-generation sequencing. Using the same strategy, the frequency of insertions/deletions was determined for the top-4 genomic off-target locations as predicted by the design tool. Typically, we observed an on-target targeting efficiency between 8 and 55%, while for off-target locations the observed indel frequency was below 0.005% (Figure 1c).

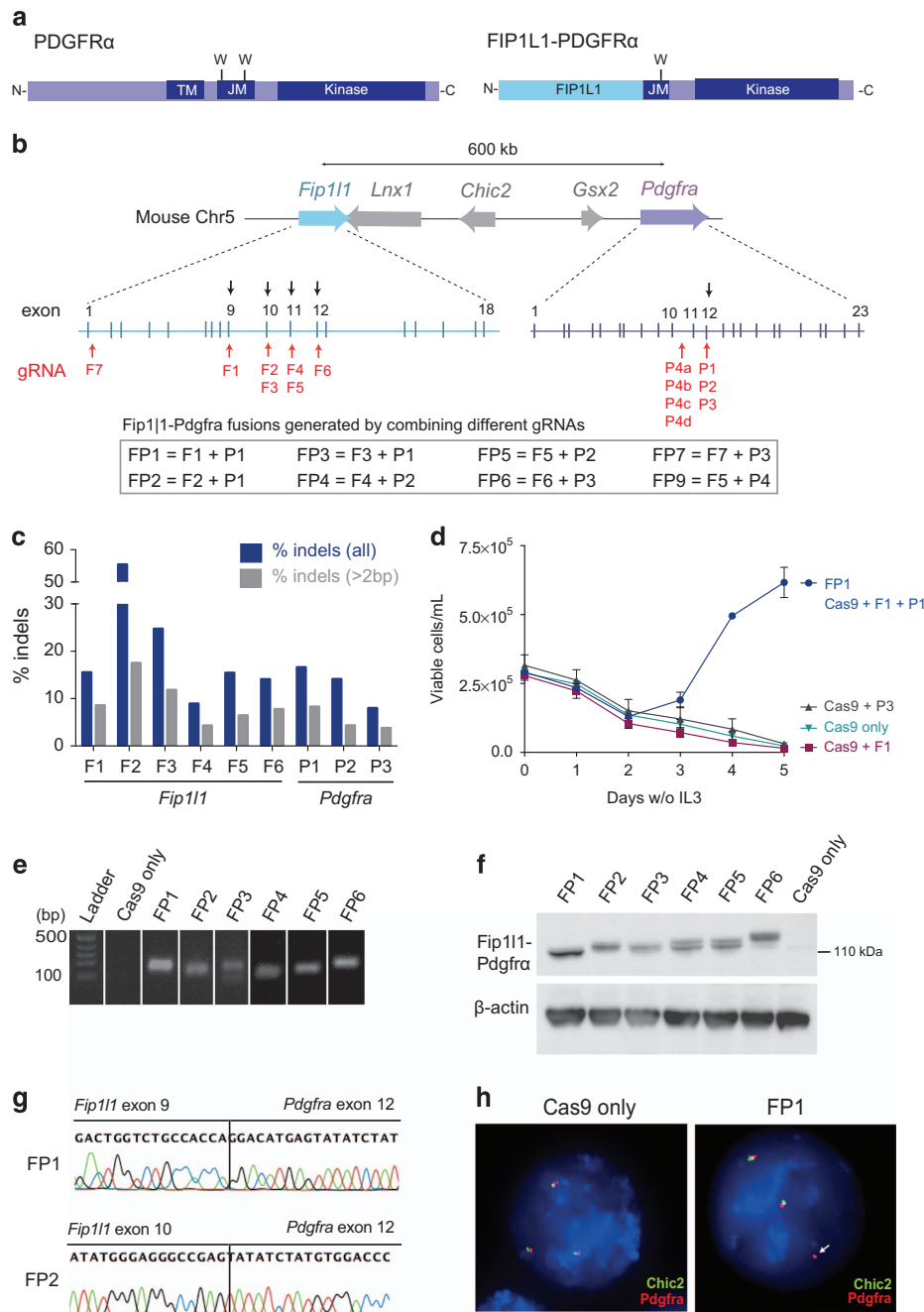
To generate various *Fip111–Pdgfra* fusion genes (designated FP1 to FP6), we combined a gRNA targeting an exon of *Fip111* with a gRNA targeting exon 12 of *Pdgfra*. Upon IL-3 removal, only Ba/F3 cells that had generated an oncogenic *Fip111–Pdgfra* fusion protein were able to survive and proliferate in the absence of IL-3 (Figure 1d). The presence of the fusion gene and protein was confirmed by PCR and western blotting, respectively (Figures 1e and f).

Single cell clones were generated from the Ba/F3 cells harboring the six different *Fip111–Pdgfra* fusions using semi-solid growth medium (Clonacell, Stem Cell Technologies, Vancouver, BC, Canada). The region spanning the fusion between *Fip111* and *Pdgfra* was amplified by PCR and sequenced using Sanger sequencing (Figure 1g). Fluorescence *in situ* hybridization (FISH) confirmed the presence of the deletion between *Fip111* and *Pdgfra* on one copy of mouse chromosome 5 and we consistently only observed heterozygous deletions (Figure 1h). These data confirm that the *Fip111–Pdgfra* fusion gene can be generated by CRISPR/Cas genome editing and that expression of the fusion gene is sufficient to transform Ba/F3 cells in a similar manner to ectopic overexpression of the recombinant *FIP1L1–PDGFRA* fusion.

We showed previously that the *Fip111* portion of the *Fip111–Pdgfra* fusion protein is dispensable for its transforming capacities.<sup>10</sup> We have to note, however, that this was only studied under overexpression conditions.<sup>10</sup> Using the genome editing strategy, we now generated a fusion between *Fip111* exon 1 and *Pdgfra* exon 12 (designated FP7), using gRNAs F7+P3 (Figure 1b). This strategy generated a fusion protein, as shown in Figure 2a, which was able to transform the cells, confirming that also with normal expression levels, the *Fip111* part is dispensable for constitutive kinase activation (Figures 2b–d).

We also showed previously that disruption of the juxtamembrane domain of *Pdgfra* (exon 12), removing one of the conserved tryptophan residues responsible for autoinhibition of the JM domain, is absolutely required for the transforming capacities of the fusion protein.<sup>10</sup> To confirm these earlier findings with more normal expression levels, we used the same genome editing strategy to generate a *Fip111–Pdgfra* fusion protein with an intact juxtamembrane domain (Figure 2e). We designed four different gRNAs targeting intron 10 of *Pdgfra* (designated P4a–d, Figure 1b), from which three gRNAs were able to generate a fusion gene in combination with a gRNA targeting *Fip111* (Figure 2f, the four different fusions are designated FP9–1 to FP9–4). However, these fusion proteins were not able to transform Ba/F3 cells (Figure 2g). These data show that *Fip111* is dispensable for the transformation capacities of the *Fip111–Pdgfra* fusion protein, and that interruption of the juxtamembrane domain is critical for the activation of the *Fip111–Pdgfra* protein. Taken together, these results show that previously obtained data with overexpression models are valid.

Next, we compared the expression and phosphorylation levels of *Fip111–Pdgfra* between the CRISPR/Cas-generated Ba/F3 cells harboring the endogenous *Fip111–Pdgfra* fusion gene and retrovirally transduced cells overexpressing *FIP1L1–PDGFRA*. Retrovirally transduced cells showed more than 10-fold higher protein expression and phosphorylation levels of *FIP1L1–PDGFRA*, as calculated by ImageJ software. We observed similar expression and phosphorylation of Stat5, which is a downstream effector of *Fip111–Pdgfra* (Figure 2h). When the cells were treated with 100 nM imatinib, the autophosphorylation of *Fip111–Pdgfra* was completely inhibited (Figure 2h). Remarkably, the EC50 values (measured after 24 h exposure to imatinib) were not significantly different between the CRISPR/Cas-generated Ba/F3 cells and retrovirally transduced cells (95% confidence intervals for the EC50 values shown in Figure 2i). These results show that, despite

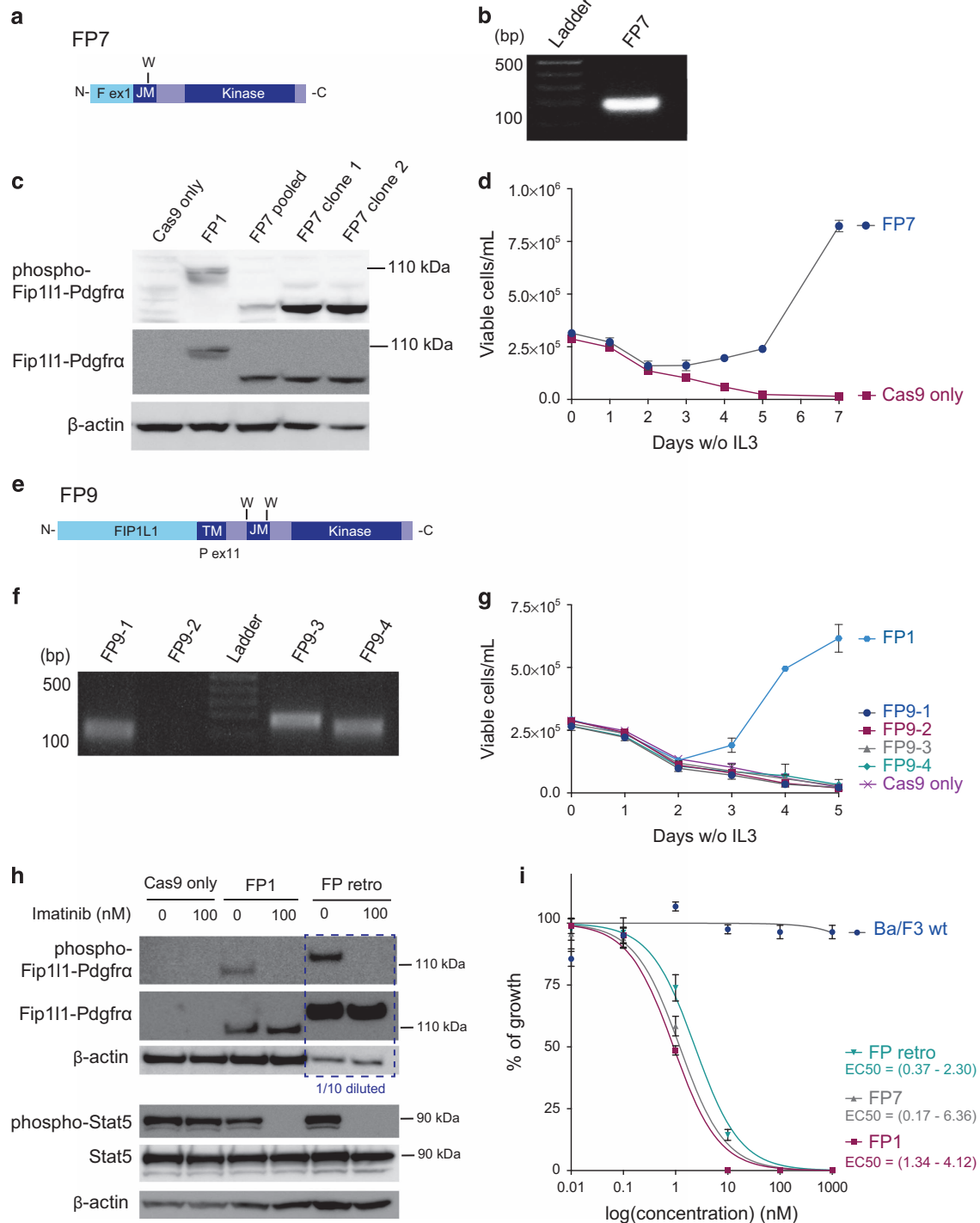


**Figure 1.** Use of CRISPR/Cas genome editing to generate Fip111-Pdgfra fusions. **(a)** Structure of PDGFR $\alpha$  and the FIP1L1-PDGFR $\alpha$  fusion protein. Formation of the fusion leads to disruption of the JM domain between two tryptophan (W) residues in PDGFR $\alpha$  (TM = transmembrane domain, JM = juxtamembrane domain). **(b)** Representation of the *Fip111* and *Pdgfra* mouse genes. Exons are indicated by vertical bars. Red arrows indicate the location of the gRNA target sites in mouse *Fip111* and *Pdgfra*. Black arrows indicate homologous sequences of breakpoints found in patients. **(c)** Efficiency of the individual gRNAs targeting *Fip111* and *Pdgfra* in Ba/F3 cells as determined by Illumina next-generation sequencing. **(d)** Growth curve showing the transforming capacities of Ba/F3 cells harboring an endogenous FIP1 fusion. Ba/F3 cells harboring a FP2-FP6 fusion had similar transformation rates (data not shown). Electroporation of only 1 gRNA targeting *Fip111* or *Pdgfra* could not transform the Ba/F3 cells. Cas9 only refers to a vector containing Cas9 without a gRNA sequence. **(e)** PCR to detect six different gene fusions in Ba/F3 cells electroporated with a vector containing Cas9 and gRNA sequences targeting *Fip111* and *Pdgfra*. Cas9 only refers to a vector containing Cas9 without a gRNA sequence. **(f)** Western blot showing six different FIP111-Pdgfra fusion proteins expressed in Ba/F3 cells. Different breakpoints in *Fip111* lead to different molecular weights. **(g)** Sequencing trace showing a fusion between *Fip111* and *Pdgfra* in Ba/F3 single cell clones of two different fusion genes (FP1 and FP2). **(h)** FISH on Ba/F3 cells electroporated with empty vector or with vectors containing *Fip111-Pdgfra* gRNAs. The white arrow indicates loss of one copy of *Chic2*, a gene in the deleted region between *Fip111* and *Pdgfra*.

the more than 10-fold difference in protein expression levels, the sensitivity of the cells to imatinib was not significantly altered.

Overall, these data show that it is feasible to generate fusion genes in the IL3-dependent Ba/F3 cell line using CRISPR/Cas

genome editing, and that these fusion genes can transform the cells to IL3-independent growth. We also conclude that no major differences were observed between Ba/F3 cells overexpressing FIP1L1-PDGFR $\alpha$  from a retroviral construct and CRISPR/Cas



**Figure 2.** Study of the properties of the Fip111-Pdgfra fusion protein. **(a)** Structure of the FP7 fusion. Break points are located in *Fip111* exon 1 and *Pdgfra* exon 12 (W = tryptophan residue, TM = transmembrane domain, JM = juxtamembrane domain). **(b)** PCR to detect the FP7 fusion in Ba/F3 cells. **(c)** Western blot showing expression of the FP7 fusion protein in Ba/F3 cells after electroporation of gRNAs targeting *Fip111* exon 1 and *Pdgfra* exon 12. **(d)** Growth curve showing the transforming capacities of Ba/F3 cells harboring an endogenous FP7 fusion. **(e)** Structure of the FP9 fusion. Break points are located in *Fip111* exon 9 and *Pdgfra* exon 11 (W = tryptophan residue, TM = transmembrane domain, JM = juxtamembrane domain). **(f)** PCR to detect four different FP9 fusions with four different gRNAs targeting the upstream region of *Pdgfra* exon 11. **(g)** Growth curve of Ba/F3 cells harboring an endogenous FP1 or FP9 fusion. **(h)** Western blot showing the effects of Imatinib on the Fip111-Pdgfra fusion protein. Ba/F3 cells harboring an endogenous FP1 fusion (FP1) and Ba/F3 cells expressing a human FIP1L1-PDGFR $\alpha$  cDNA (FP retro) were treated for 90 min with 0 or 100 nM Imatinib. On the blots showing expression of (p)-Fip111-Pdgfra, a 1/10 dilution of FP retro is shown. Difference in molecular weight of Fip111-Pdgfra is due to differences in molecular weight between the mouse and human fusion proteins. **(i)** Dose response curve for Imatinib. EC<sub>50</sub> values are represented by 95% confidence intervals.

engineered cells. The cells equally activated the downstream effector Stat5, and were equally sensitive to imatinib, despite the huge differences in protein expression levels. Moreover, previous data on the mechanism of activation were confirmed in the CRISPR/Cas engineered cells. Our data demonstrate an important application of the CRISPR/Cas genome editing tool, which makes it possible to study the oncogenic properties of activated tyrosine kinases without the need for ectopic overexpression.

## CONFLICT OF INTEREST

The authors declare no conflict of interest.

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